

Tavazza.ST25.txt  
SEQUENCE LISTING

<110> ENEA-Ente per le Nuove Tecnologie e l'Ambiente  
Consiglio Nazionale delle Ricerche

<120> Method for the preparation of transgenic plants characterised by  
Geminivirus lasting resistance

<130> PCT25622

<140> RM2003A000242

<141> 2003-05-19

<150> RM2003A000242

<151> 2003-05-19

<160> 12

<170> PatentIn version 3.2

<210> 1

<211> 630

<212> DNA

<213> Geminivirus TYLCSV

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ctcatccaat tcgaaggaaa atacaattgt accaatcaac gattcttcga cctgggtatcc 240  
ccaaccaggt cagcacattt ccatccgaac attcaggagg cttaaactgag ctccgacgtc 300  
aagtcctata tcgacaagga cggagatggt cttgaatggg gtactttcca gatcgacgga 360  
cgatctgcta ggggaggaca acagacagcc aacgacgctt acgcaaaggc aattaacgca 420  
ggaagtaagt cgcaggctct tgatgtaatt aaagaattag cgcctagaga ttacgttcta 480  
cattttcata atataaatag taatttagat aagggtttcc aggtgcctcc ggcaccttat 540  
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aca tac ccc aag tgt gac tta act aag gag aat gca ttg tcc cag ata 96  
Pagina 1

Thr Tyr Pro Lys Cys Asp Leu Thr Lys Glu Asn Ala Leu Ser Gln Ile  
 20 25 30  
 144  
 act aac ttg caa act ccc act aac aag ttg ttc att aag att tgt agg  
 Thr Asn Leu Gln Thr Pro Thr Asn Lys Leu Phe Ile Lys Ile Cys Arg  
 35 40 45  
 192  
 gaa ctt cat gag aat gga gaa cca cat ctt cat atc ttg ata cag ttc  
 Glu Leu His Glu Asn Gly Glu Pro His Leu His Ile Leu Ile Gln Phe  
 50 55 60  
 240  
 gaa ggc aag tat aac tgc acc aac caa cgt ttc ttt gac ctt gtg tcc  
 Glu Gly Lys Tyr Asn Cys Thr Asn Gln Arg Phe Phe Asp Leu Val Ser  
 65 70 75 80  
 288  
 cct acc aga tca gcc cat ttt cat cca aac atc cag ggt gct aag tcg  
 Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser  
 85 90 95  
 336  
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 Ser Ser Asp Val Lys Ser Tyr Ile Asp Lys Asp Gly Asp Val Leu Glu  
 100 105 110  
 384  
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 Trp Gly Thr Phe Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln  
 115 120 125  
 432  
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 Thr Ala Asn Asp Ala Tyr Ala Lys Ala Ile Asn Ala Gly Ser Lys Ser  
 130 135 140  
 480  
 cag gca ctt gac gta atc aaa gag tta gct cct agg gat tat gtt ctt  
 Gln Ala Leu Asp Val Ile Lys Glu Leu Ala Pro Arg Asp Tyr Val Leu  
 145 150 155 160  
 528  
 cat ttc cat aac atc aac agc aat ttg gac aaa gtg ttc caa gtg cca  
 His Phe His Asn Ile Asn Ser Asn Leu Asp Lys Val Phe Gln Val Pro  
 165 170 175  
 576  
 ccg gct cct tac gtt tca cct ttc tta agt tct tca ttt gat cag gtt  
 Pro Ala Pro Tyr Val Ser Pro Phe Leu Ser Ser Ser Phe Asp Gln Val  
 180 185 190  
 624  
 cca gat gag ctt gag cat tgg gtg tcc gaa aac gtt atg gac gcc gca  
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Thr Asn Leu Gln Thr Pro Thr Asn Lys Leu Phe Ile Lys Ile Cys Arg  
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 Glu Leu His Glu Asn Gly Glu Pro His Leu His Ile Leu Ile Gln Phe  
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 Glu Gly Lys Tyr Asn Cys Thr Asn Gln Arg Phe Phe Asp Leu Val Ser  
 65 70 75 80  
 Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser  
 85 90 95  
 Ser Ser Asp Val Lys Ser Tyr Ile Asp Lys Asp Gly Asp Val Leu Glu  
 100 105 110  
 Trp Gly Thr Phe Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln  
 115 120 125  
 Thr Ala Asn Asp Ala Tyr Ala Lys Ala Ile Asn Ala Gly Ser Lys Ser  
 130 135 140  
 Gln Ala Leu Asp Val Ile Lys Glu Leu Ala Pro Arg Asp Tyr Val Leu  
 145 150 155 160  
 His Phe His Asn Ile Asn Ser Asn Leu Asp Lys Val Phe Gln Val Pro  
 165 170 175  
 Pro Ala Pro Tyr Val Ser Pro Phe Leu Ser Ser Ser Phe Asp Gln Val  
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 Ala Arg  
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 <222> (1)..(630)

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 1 5 10 15

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 Thr Asn Leu Gln Thr Pro Thr Asn Lys Leu Phe Ile Lys Ile Cys Arg  
 35 40 45  
 gaa ctt cac gag aat gga gaa cca cat ctt cat atc ttg ata cag ttc 192  
 Glu Leu His Glu Asn Gly Glu Pro His Leu His Ile Leu Ile Gln Phe  
 50 55 60  
 gaa ggc aag tat aac tgc acc aac caa cgt ttc ttt gac ctt gtg tcc 240  
 Glu Gly Lys Tyr Asn Cys Thr Asn Gln Arg Phe Phe Asp Leu Val Ser  
 65 70 75 80  
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 Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser  
 85 90 95  
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 Ser Ser Asp Val Lys Ser Tyr Ile Asp Lys Asp Gly Asp Val Leu Glu  
 100 105 110  
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 Trp Gly Thr Phe Gln Ile Asp Gly Arg Ser Ala Arg Gly Gln Gln  
 115 120 125  
 aca gca aac gat gca tac gct aag gct atc aac gct gga tcc aag tca 432  
 Thr Ala Asn Asp Ala Tyr Ala Lys Ala Ile Asn Ala Gly Ser Lys Ser  
 130 135 140  
 cag gca ctt gac gta atc aaa gag tta gct cct agg gat tat gtt ctt 480  
 Gln Ala Leu Asp Val Ile Lys Glu Leu Ala Pro Arg Asp Tyr Val Leu  
 145 150 155 160  
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 His Phe His Asn Ile Asn Ser Asn Leu Asp Lys Val Phe Gln Val Pro  
 165 170 175  
 ccg gct cct tac gtt tca cct ttc tta agt tct tca ttt gat cag gtt 576  
 Pro Ala Pro Tyr Val Ser Pro Phe Leu Ser Ser Ser Phe Asp Gln Val  
 180 185 190  
 cca gat gag ctt gag cat tgg gtg tct gaa aac gtt atg gac gcc gca 624  
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 Pagina 4

Thr Asn Leu Gln Thr Pro Thr Asn Lys Leu Phe Ile Lys Ile Cys Arg  
35 40 45  
Glu Leu His Glu Asn Gly Glu Pro His Leu His Ile Leu Ile Gln Phe  
50 55 60  
Glu Gly Lys Tyr Asn Cys Thr Asn Gln Arg Phe Phe Asp Leu Val Ser  
65 70 75 80  
Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser  
85 90 95  
Ser Ser Asp Val Lys Ser Tyr Ile Asp Lys Asp Gly Asp Val Leu Glu  
100 105 110  
Trp Gly Thr Phe Gln Ile Asp Gly Arg Ser Ala Arg Gly Gly Gln Gln  
115 120 125  
Thr Ala Asn Asp Ala Tyr Ala Lys Ala Ile Asn Ala Gly Ser Lys Ser  
130 135 140  
Gln Ala Leu Asp Val Ile Lys Glu Leu Ala Pro Arg Asp Tyr Val Leu  
145 150 155 160  
His Phe His Asn Ile Asn Ser Asn Leu Asp Lys Val Phe Gln Val Pro  
165 170 175  
Pro Ala Pro Tyr Val Ser Pro Phe Leu Ser Ser Ser Phe Asp Gln Val  
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Ala Arg  
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gct	ccc	aca	gtc	cag	ggc	att	aag	agg	cga	tct	tgg	aca	tac	aga	cct	144
Ala	Pro	Thr	Val	Gln	Gly	Ile	Lys	Arg	Arg	Ser	Trp	Thr	Tyr	Arg	Pro	
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Met	Tyr	Arg	Lys	Pro	Arg	Met	Tyr	Arg	Met	Tyr	Arg	Ser	Pro	Asp	Val	
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Pro	Pro	Gly	Cys	Glu	Gly	Pro	Cys	Lys	Val	Gln	Ser	Tyr	Glu	Gln	Arg	
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gac	gat	gtg	aag	cac	acc	gga	gtt	gtt	cgt	tgc	gtt	tct	gat	gtg	act	288
Asp	Asp	Val	Lys	His	Thr	Gly	Val	Val	Arg	Cys	Val	Ser	Asp	Val	Thr	
				85					90					95		
aga	ggg	tca	ggg	atc	act	cac	agg	gtg	gga	aag	cgt	ttc	tgt	att	aag	336
Arg	Gly	Ser	Gly	Ile	Thr	His	Arg	Val	Gly	Lys	Arg	Phe	Cys	Ile	Lys	
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tct	att	tac	ata	ttg	ggg	aag	atc	tgg	atg	gac	gag	aat	atc	aag	aaa	384
Ser	Ile	Tyr	Ile	Leu	Gly	Lys	Ile	Trp	Met	Asp	Glu	Asn	Ile	Lys	Lys	
		115					120					125				
cag	aat	cac	act	aat	cag	gtt	atg	ttc	ttt	ctt	gtg	cga	gat	cga	aga	432
Gln	Asn	His	Thr	Asn	Gln	Val	Met	Phe	Phe	Leu	Val	Arg	Asp	Arg	Arg	
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Asp	Asn	Glu	Pro	Ser	Thr	Ala	Thr	Val	Lys	Asn	Asp	Leu	Arg	Asp	Arg	
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Tyr	Gln	Val	Met	Arg	Lys	Phe	His	Ala	Thr	Val	Val	Gly	Gly	Pro	Ser	
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gga	atg	aaa	gag	caa	tgt	ctt	ctg	aaa	aga	ttc	ttt	aag	atc	aac	act	624
Gly	Met	Lys	Glu	Gln	Cys	Leu	Leu	Lys	Arg	Phe	Phe	Lys	Ile	Asn	Thr	
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His	Val	Val	Tyr	Asn	His	Gln	Glu	Gln	Ala	Lys	Tyr	Glu	Asn	His	Thr	
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Glu	Asn	Ala	Leu	Leu	Leu	Tyr	Met	Ala	Cys	Thr	His	Ala	Ser	Asn	Pro	
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Val	Tyr	Ala	Thr	Leu	Lys	Ile	Arg	Ile	Tyr	Phe	Tyr	Asp	Ala	Val	Thr	
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Asn																

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 35 40 45

Met Tyr Arg Lys Pro Arg Met Tyr Arg Met Tyr Arg Ser Pro Asp Val  
 50 55 60

Pro Pro Gly Cys Glu Gly Pro Cys Lys Val Gln Ser Tyr Glu Gln Arg  
 65 70 75 80

Asp Asp Val Lys His Thr Gly Val Val Arg Cys Val Ser Asp Val Thr  
 85 90 95

Arg Gly Ser Gly Ile Thr His Arg Val Gly Lys Arg Phe Cys Ile Lys  
 100 105 110

Ser Ile Tyr Ile Leu Gly Lys Ile Trp Met Asp Glu Asn Ile Lys Lys  
 115 120 125

Gln Asn His Thr Asn Gln Val Met Phe Phe Leu Val Arg Asp Arg Arg  
 130 135 140

Pro Tyr Gly Thr Ser Pro Met Asp Phe Gly Gln Val Phe Asn Met Phe  
 145 150 155 160

Asp Asn Glu Pro Ser Thr Ala Thr Val Lys Asn Asp Leu Arg Asp Arg  
 165 170 175

Tyr Gln Val Met Arg Lys Phe His Ala Thr Val Val Gly Gly Pro Ser  
 180 185 190

Gly Met Lys Glu Gln Cys Leu Leu Lys Arg Phe Phe Lys Ile Asn Thr  
 195 200 205

His Val Val Tyr Asn His Gln Glu Gln Ala Lys Tyr Glu Asn His Thr  
 210 215 220

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Asn

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 Arg Ser Gly Arg Phe Ser Ile Lys Ala Lys Asn Tyr Phe Leu Thr Tyr  
 5 10 15

ccc aaa tgt gat tta aca aaa gaa aat gca ctt tcc caa ata aca aac 152  
 Pro Lys Cys Asp Leu Thr Lys Glu Asn Ala Leu Ser Gln Ile Thr Asn  
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 Leu Gln Thr Pro Thr Asn Lys Leu Phe Ile Lys Ile Cys Arg Glu Leu  
 35 40 45 50

cat gaa aat ggg gaa cct cat ctc cat att ttg atc caa ttc gaa gga 248  
 His Glu Asn Gly Glu Pro His Leu His Ile Leu Ile Gln Phe Glu Gly  
 55 60 65

aaa tac aat tgt acc aat caa cga ttc ttc gac ctg gta tcc cca acc 296  
 Lys Tyr Asn Cys Thr Asn Gln Arg Phe Phe Asp Leu Val Ser Pro Thr  
 70 75 80

agg tca gca cat ttc cat ccg aac att cag gga gct aaa tcg agc tcc 344  
 Arg Ser Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser Ser Ser  
 85 90 95

gac gtc aag tcc tat atc gac aag gac gga gat gtt ctt gaa tgg ggt 392  
 Asp Val Lys Ser Tyr Ile Asp Lys Asp Gly Asp Val Leu Glu Trp Gly  
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act ttc cag atc gac gga cga tct gct agg gga gga caa cag aca gcc 440  
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Glu Gly Lys Tyr Asn Cys Thr Asn Gln Arg Phe Phe Asp Leu Val Ser  
 65 70 75 80

Pro Thr Arg Ser Ala His Phe His Pro Asn Ile Gln Gly Ala Lys Ser  
 85 90 95

Ser Ser Asp Val Lys Ser Tyr Ile Asp Lys Asp Gly Asp Val Leu Glu  
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 <223> Primer for PCR C4 mutagenesis

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<210> 11

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